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WHAT IS CLAIMED IS:

- 1. Isolated polynucleotide from coryneform bacteria containing a polynucleotide sequence selected from the group consisting of
 - a) a polynucleotide which is at least 70% identical to a polynucleotide which encodes a polypeptide containing the amino acid sequence of SEQ ID NO: 2,
- b) a polynucleotide which encodes a polypeptide which contains an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID NO:2,
 - c) a polynucleotide which is complementary to the polynucleotides of a) or b), and
 - e) a polynucleotide dontaining at least 15 successive bases of the polynucleotide sequence of a), b) or c).
- The polynucleotide according to claim 1,
 wherein the polynucleotide is DNA replicable in coryneform bacteria.
 - 3. The polynucleotide according to claim 2 which is recombinant DNA.
- 4. The polynucleotide according to claim 1, wherein the polynucleotide is an RNA.
 - 5. The polynucleotide according to claim 2, containing the nucleic acid sequence represented in SEQ ID NO:1.
 - 6. The replicable DNA according to claim 2, containing

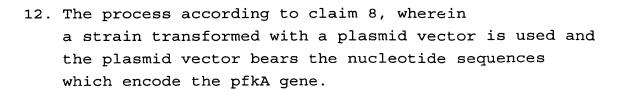
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- (i) the nucleotide sequence shown in SEQ ID NO:1, or
- (ii) at least one sequence which matches the sequence(i) within the degeneration range of the genetic code, or
- 5 (iii) at least one sequence which hybridises with the complementary sequence to sequence (i) or (ii) and optionally
 - (iv) functionally neutral sense mutations in (i).
 - 7. The polynucleotide sequence according to claim 2 which encodes a polypeptide which contains the amino acid sequence shown in SEQ ID NO:2.
 - 8. A process for the fermentative production of L-amino acids, in particular L-lysine, comprising the following steps:
 - a) fermentation of L-amino acid producing coryneform bacteria in which at least the pfkA gene or nucleotide sequences coding therefor is/are amplified,
 - b) accumulation of the L-amino acid in the medium or in the cells of the bacteria and
 - c) isolation of the L-amino acid.
 - 9. The process according to claim 8 wherein the gene or sequences are amplified by overexpression.
- 10. The process according to claim 8, wherein
 25 bacteria are used in which further genes of the
 biosynthetic pathway of the desired L-amino acid are
 additionally amplified.
 - 11. The process according to claim 8, wherein bacteria are used in which the metabolic pathways which reduce the formation of L-lysine are at least partially suppressed.

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- 5 13. The process according to one of claims 8 to 12, wherein coryneform bacteria are used which produce L-lysine.
 - 14. The process according to claim 8, wherein bacteria are fermented for the production of lysine in which one or more of the genes selected from the group
 - a) the dapA gene which encodes dihydropicolinate synthase,
 - b) the pyc gene, which encodes pyruvate carboxylase,
 - c) the tpi gene, which encodes triosephosphate isomerase,
 - d) the dapE gene, which encodes succinyldiaminopimelate desuccinylase,
 - e) the gap gene, which encodes glyceraldehyde3-phosphate dehydrogenase,
- f) the pgk gene, which encodes 3-phosphoglycerate kinase, and
 - g) the lysE gene, which encodes for lysine export, is/are simultaneously amplified.
- 15. The process according to claim 14, wherein the gene(s) is/are amplified by overexpression.
 - 16. The process according to claim 11, wherein bacteria are fermented for the production of L-lysine in which one or more of the genes selected from the group consisting of

- - a) the pck gene, which encodes phosphoenolpyruvate carboxykinase, and
 - b) the pgi gene, which encodes glucose 6-phosphate isomerase,
- is/are simultaneously attenuated. 5
 - 17. The process according to one of claims 8-12 or 14-15, wherein microorganisms of the genus Corynebacterium glutamicum are used.
 - 18. A process for production of DNA of genes which encode phosphofructokinase comprising employment of polynucleotide sequences according to claim 1 as primers in a polymerase chain reaction.
 - 19. A hybridization probe comprising a polynucleotide sequence according to claim 1.

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